

--1. (Amended) An isolated coryneform bacterium in which L-arginine biosynthesis is not repressed by an *argR* gene in a normal manner, and which has L-arginine producing ability.

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2. (Amended) The isolated coryneform bacterium according to Claim 1, wherein L-arginine biosynthesis is not repressed by the *argR* gene in a normal manner due to disruption of the *argR* gene which has the nucleotide sequence shown in SEQ ID NO:17 or has such a degree of homology that it should cause homologous recombination with the nucleotide sequence shown in SEQ ID NO:17, and which is on a chromosome of the bacterium.

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3. (Amended) The isolated coryneform bacterium according to Claim 2, wherein the *argR* gene encodes the amino acid sequence shown in SEQ ID NO:18 or an amino acid sequence which is encoded by an *argR* gene having such a degree of homology that it should cause homologous recombination with the *argR* gene coding for the amino acid sequence shown in SEQ ID NO:18.--

Please add the following new claims:

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5. (New) The isolated coryneform bacterium of Claim 1, wherein said coryneform bacterium belongs to a species selected from the group consisting of

Corynebacterium acetoacidophilum,

Corynebacterium acetoglutamicum,

Corynebacterium alkanolyticum,

Corynebacterium callunae,

Corynebacterium glutamicum,

Corynebacterium lilium,

Corynebacterium melassecola,

Corynebacterium thermoaminogenes,
Corynebacterium herculis,
Brevibacterium divaricatum,
Brevibacterium flavum,
Brevibacterium immariophilum,
Brevibacterium lactofermentum,
Brevibacterium roseum,
Brevibacterium saccharolyticum,
Brevibacterium thiogenitalis,
Brevibacterium album,
Brevibacterium cerinum, and
Microbacterium ammoniaphilum.

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6. (New) The isolated coryneform bacterium of Claim 2, wherein said coryneform bacterium belongs to a species selected from the group consisting of

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Corynebacterium acetoacidophilum,
Corynebacterium acetoglutamicum,
Corynebacterium alkanolyticum,
Corynebacterium callunae,
Corynebacterium glutamicum,
Corynebacterium lilium,
Corynebacterium melassecola,
Corynebacterium thermoaminogenes,
Corynebacterium herculis,

Brevibacterium divaricatum,
Brevibacterium flavum,
Brevibacterium immariophilum,
Brevibacterium lactofermentum,
Brevibacterium roseum,
Brevibacterium saccharolyticum,
Brevibacterium thiogenitalis,
Brevibacterium album,
Brevibacterium cerium, and
Microbacterium ammoniaphilum.

7. (New) The isolated coryneform bacterium of Claim 3, wherein said coryneform bacterium belongs to a species selected from the group consisting of

Corynebacterium acetoacidophilum,
Corynebacterium acetoglutamicum,
Corynebacterium alkanolyticum,
Corynebacterium callunae,
Corynebacterium glutamicum,
Corynebacterium lilyum,
Corynebacterium melassecola,
Corynebacterium thermoaminogenes
Corynebacterium herculis,
Brevibacterium divaricatum,
Brevibacterium flavum,

Brevibacterium immariophilum,
Brevibacterium lactofermentum,
Brevibacterium roseum,
Brevibacterium saccharolyticum,
Brevibacterium thiogenitalis,
Brevibacterium album,
Brevibacterium cerinum, and
Microbacterium ammoniophilum.

Sul D 8. (New) The isolated coryneform bacterium of Claim 1, wherein said coryneform bacterium is resistant to a compound selected from the group consisting of sulfa drugs, 2-thiazolealanine, and α -amino- β -hydroxyvaleric acid.

Sul D 9. (New) The isolated coryneform bacterium of Claim 2, wherein said coryneform bacterium is resistant to a compound selected from the group consisting of sulfa drugs, 2-thiazolealanine, and α -amino- β -hydroxyvaleric acid.

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Cont 10. (New) The isolated coryneform bacterium of Claim 3, wherein said coryneform bacterium is resistant to a compound selected from the group consisting of sulfa drugs, 2-thiazolealanine, and α -amino- β -hydroxyvaleric acid.

Sul D 11. (New) The isolated coryneform bacterium of Claim 1, wherein said coryneform bacterium exhibits auxotrophy for a compound selected from the group consisting of L-histidine, L-proline, L-threonine, L-isoleucine, L-methionine, and L-tryptophan.

Sul D 12. (New) The isolated coryneform bacterium of Claim 2, wherein said coryneform bacterium exhibits auxotrophy for a compound selected from the group consisting of L-histidine, L-proline, L-threonine, L-isoleucine, L-methionine, and L-tryptophan.

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13. (New) The isolated coryneform bacterium of Claim 3, wherein said coryneform bacterium exhibits auxotrophy for a compound selected from the group consisting of L-hisitidine, L-proline, L-threonine, L-isoleucine, L-methionine, and L-tryptophan.

14. (New) The isolated coryneform bacterium of Claim 1, wherein said coryneform bacterium is resistant to a compound selected from the group consisting of ketomalonic acid, fluoromalonic acid, and monofluoroacetic acid.

15. (New) The isolated coryneform bacterium of Claim 2, wherein said coryneform bacterium is resistant to a compound selected from the group consisting of ketomalonic acid, fluoromalonic acid, and monofluoroacetic acid.

16. (New) The isolated coryneform bacterium of Claim 3, wherein said coryneform bacterium is resistant to a compound selected from the group consisting of ketomalonic acid, fluoromalonic acid, and monofluoroacetic acid.

17. (New) The isolated coryneform bacterium of Claim 1, wherein said coryneform bacterium is resistant to a compound selected from the group consisting of arginol and X-guanidine, wherein X is derived from a fatty acid or aliphatic chain.

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18. (New) The isolated coryneform bacterium of Claim 2, wherein said coryneform bacterium is resistant to a compound selected from the group consisting of arginol and X-guanidine, wherein X is derived from a fatty acid or aliphatic chain.

19. (New) The isolated coryneform bacterium of Claim 3, wherein said coryneform bacterium is resistant to a compound selected from the group consisting of arginol and X-guanidine, wherein X is derived from a fatty acid or aliphatic chain.

Add C27

SUPPORT FOR THE AMENDMENTS

Applicants have amended Claim 1 to specify that the arginine biosynthesis is not repressed due to disruption of an *argR* gene. Support for this amendment can be found on page 4, lines 17-21, and page 5, lines 10-11. Applicants have amended Claim 2 to recite that the *argR* gene has the nucleotide sequence shown in SEQ ID NO:17 or has such a degree of homology that it should cause homologous recombination with the nucleotide sequence shown in SEQ ID NO:17. Support for this amendment can be found on page 13, line 27, to page 14, line 22, of the specification. Claim 3 has been amended to replace the phrase “showing homology to the amino acid sequence” with the phrase “is encoded by an *argR* gene having such a degree of homology that it should cause homologous recombination with the *argR* gene coding for the amino acid sequence shown in SEQ ID NO:18.” Support for this amendment can also be found on page 13, line 27, to page 14, line 22, of the specification.

Applicants have added new Claims 5-7. Support for new Claim 5 can be found on page 6, line 16, to page 7, line 17, of the specification. Support for Claims 8-19 can be found on page 7, line 18, to page 8, line 9, of the specification.

No new matter has been added. Claims 1-3 and 5-19 are active in this application.

REMARKS

At the outset, Applicants wish to thank Examiner Fronda for indicating that Claims 1-3 are free of the prior art. Applicants submit that in view of the present amendments that Claims 1-3 and 5-19 meet all the requirements of 35 U.S.C. § 112 and are, thus, in condition for allowance.